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GenCore version 5.1.6
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September 26, 2003, 10:11:26; Search time 1905 Seconds (without alignments) 10136.138 Million cell updates/sec US-10-045-116-1
472
1 AGCCACCACCAGTGAGCCT.....ACGTTCCTGGAACTCAAGCA 472 5777422 2888711 seqs, 20454813386 residues Total number of hits satisfying chosen parameters: OM nucleic - nucleic search, using sw model Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries IDENTITY_NUC Gapop 10.0 , Gapext 1.0 em_vi:*
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description					Sequence	AR266427 Sequence	AX259954 Sequence	AX262359 Sequence	Acousass Homo sapi X62151 H.sapiens c	A37261 Sequence 1	M59255 Human carci	AX705383 Sequence	X98312 H.saniens c	AC005797 Homo sapi	AX705384 Sequence	M60963 Himan cardi	AC005626 Homo sapi	AC011513 Homo sapi	AC004559 Homo sapi	AF110325 Homo sapi	AC005955 Homo sapi	AC005392 Homo sapi	X67277 H.sapiens B	AC004785 Homo sapi	AC110916 Rattus no	AR134886 Sequence	AR182305 Sequence	AC005797 Homo sapi	AC140257 Mus muscu	ACL344/5 Mus muscu AC020516 Homo sani	AC005955 Homo sapi	M22433 Homo sapien	ACU/9525 Mus muscu M83340 Mouse proce	AC079497 Mus muscu	11 Mus musc 70 Rattus n			10 E 8 C	Linear FAT 04-APR-2003				<pre>Vertebrata; Euteleostomi; ; Hominidae; Homo.</pre>		s of colon cancer	
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Pred. No. 6.3e-141;
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Richards, C.Ann. and Huber, B.
Transcriptional regulatory sequence of
expression targeting
Patent: US 6194211-A 1 27-FEB-2001;
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Patent: US 6337209-A 4 08-JAN-2002;
Location/Qualifiers
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PRI 29-MAY-1996

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Schrewe, H., Thompson, J., Bona, M., Hefta, L.J., Maruya, A., Hassauer, M., Shively, J.E., von Kleist, S. and Zimmermann, W. Cloning of the complete gene for carcinoembryonic antigen: analysis of its promoter indicates a region conveying cell type-specific
                                                          (bases 1 to 11288)
Richards, C.A., Austin, E.A. and Huber, B.E.
Transcriptional regulatory sequences of carcinoembryonic antigen:
identification and use with cytosine deaminase for tumor-specific
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The transcriptional control region of the human carcinoembryonic antigen gene: DNA sequence and homology studies
DNA Seq. 4 (3), 185-196 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (24-FEB-1993) Richards C. A., Burroughs Wellcome Co., cell Biology, 3030 Cornwallis Rd, Research Triangle Park, North Carolina, USA, 27709
Overlapping sequence: U17131.
Location/Qualifiers
                                                                                                                                     10714 GCAGACCAGACAGTCACAGCGCTTGACAAAACGTTCCTGGAACTCAAGC 10764
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Hum. Gene Ther. 6 (7), 881-893 (1995)
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2106 .2156
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Richards, C.A.
Direct Submission
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Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0174861-A 1 11-OCT-2001;
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/db_xref="taxon:9606"
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/note="unnamed protein product"
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/db_xref="G1:16542050"
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6746. .6887
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/rpt_type=DISPERSED
10694. .11288
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10694. 10867
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Henderson,D.R. and Yu,D.C.
Target cell-specific adenoviral vectors containing E3 and methods of use thereof
Patent: US 6495130-A 10 17-DEC-2002;
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/mol_type="genomic DNR"
/db_xecf="texon:32630"
/note="CEA-TRE"
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                                                                     GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGAACCCTGCTGGG
                                                                               1 AGCCACCACCAGIGAGCCITITICIAGCCCCCAGAGCCACCICIGICACCITCCIGIIG
                                            TTTCTCTCTCTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCCAAGGACAGAACACAG
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100.0%; Pred. No. 7.5e-141;
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Patent: WO 0173093-A 14 04-0CT-2001,
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Location/Qualifiers
1. .15056
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TITCTCTGTCACAAAAGGAAAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
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94598, USA
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Submitted (03-NOV-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 39707)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted (26-NOV-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
5 (bases 1 to 39707)
DOE Joint Genome Institute and Stanford Human Genome Center.
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AC008999.7 GI:15281189
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DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Submitted (23-AUG-2001) DOE Joint Genome Institute, 28
Drive, Walnut Creek, CA 94598, USA
On Aug 23, 2001 this sequence version replaced gi:1107
Draft Sequence Produced by DOE Joint Genome Institute
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Mammalia; Eutheria; Primates; Catarrhin; Hominidae;
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Filishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.
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/db_xref="taxon:9606"
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DOE Joint Genome Institute.
Direct Submission
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Match 96.6%;
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Cell_type="EBV-immortalized lymphoblast"
/clone_lib="EcoRI segment of cosmid; c103.2 from Alzheimer
6 cosmid library"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4137)
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Submitted (12-SEP-1991) T. Barnett, Miles, Inc., 400 Morgan Lane,
West Haven, CT 06516, USA
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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 /chromosome="19"
/clone="LLNLR-269B9"
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/translation="MESPAPPHRWCIPWQRLLLIASLLTFWNPPTTARLTIESTPFN VAEGREVLLVHNLEQHLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIY PNASLLIQUIQUITQNPTGFYTLHVIKSDLVNEEATGQFRVYRE" 3500
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            /codon_start=1
/product="carinoembryonic antigen"
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Pred. No. 5.4e-136;
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IMP CANCER RES TECH (GB)
Location/Qualifiers
                                               /protein_id="CAA44076.1"
/db_xref="G1:1877203"
/db_xref="SPTREMBL:P78448"
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/organism="unidentified"
/mol_type="genomic DNA"
/db.xref="taxon:32644"
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Sequence 1 from Patent W09404196
.2680,3605.
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Vile, R.G. and Hart, I.R.
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/gene="CEA"
/note="G00-119-054"
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Homota; Metazoa; Chordata; Catarrhini; Hominidae; Euteleostomi;
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                                                                                       4;
                                     91.6%; Score 432.4; DB 6; Length 3281;
llarity 98.9%; Pred. No. 2e-128;
Conservative 0; Mismatches 1; Indels 4;
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M59255 M31966
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90258861
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/clone="cosCBA1"
1659. 1832
/gene="CEA"
/note="G00-119-054"
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Method and nucleic acids for the analysis of colon cancer
Patent: WO 03014388-A 52 20-FEB-2003;
                                                                        Length 3281;
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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                                                                                              0; Mismatches
                             610
                                                                     Score 432.4;
Pred. No. 2e-
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/note="G00-119-054"
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Location/Qualifiers
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PRI 30-JUN-1997

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (24-MAY-1996) W. Zimmermann, Albert-Ludwigs-University,
Institute of Immunobiology, Stefan-Meier-Strasse 8, D-79104
                                                                                                                                                                                                                                                                                                                                                    X98312.1 GI:1524061 carcinoembryonic antigen family member carcinoembryonic autigen;
                                                               Thompson, J., Seitz, M., Chastre, E., Ditter, M., Aldrian, C.,
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Down-regulation of carcinoembryonic antigen family member
expression is an early event in colorectal tumorigenesis
Cancer Res. 57 (9), 1776-1784 (1997)
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H.sapiens carcinoembryonic antigen
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/tissue_type="placenta"
/dev_stage="embyro"
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/chromosome="19"
/map="q13.2"
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/db_xref="GI:4378976"
/translation="M"
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/gene="CGM2"
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/gene="CGM2"
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                    ACCITCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGGACCCTGCTGGTTTCTCTGTCA
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Wethod and nucleic acids for the analysis
Patent: WO 03014388-A 74 20-FEB-2003;
Epigenomics AG (DE)
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="chemically treated genom:
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56.1%; Score 264.8; DB 9; Length 645; ularity 80.3%; Pred. No. 3.3e-74; Conservative 0; Mismatches 62; Indels 32; Gaps			rn.			TITCICICICAC-AAGGGAAATAAICCCCCIGGIGIGACAAGACCCAAGGCCAAGGACACAG		CATAGGICAGCACIGGGAAAGGIIGGIIGIIIIIIIIIII		370 GCTACTCAAAGCTTTGTATCGGGAACTGAATATAGACAAAAAGGGAAAGAGAGAG				GGACCATGTGATCTTGGAAAGTGCTCCTGCCCTGGGAGGGA	AGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAA-AACGTTCCTGGAACTCAAGC 471	AGGACAGCAGAGGTGACAGTCACAGCAGCCCTGACAAGAGAGTTCCTGGAGCCCAAGC 607
tch al Simi 384;	1 A	155 A	61 G	215 Ġ	121 T	251 T	181 C.	310 C	241 G	370 G	295 AJ	430 A	355 GZ	490 GG	415 AG	550 AG
Query Match Best Local Similarity Matches 384; Conser	QY	QQ	QY	qq	QY	qa	OY	qa	QY	qq	Qy 2	Db 4	Qy 3	Db 4	0Σ 4	Db 5

Search completed: September 26, 2003, 13:06:57 Job time: 1910 secs

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Carcinoembryonic a
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DNA sequence of co
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Human carcinoembry
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Schuur ER;

Henerson DR, Lamparski HG,

WPI; 1998-495862/42

(CALY-) CALYDON INC

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GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the human carcinoembryonic antigen transcriptional regulatory element (CEA-TRE). It was isolated from human genomic DNA by PCR (see AAV52945-46). The CEA-TRE is capable of mediating gene expression specific to cells capable of expressing CEA or capable of CRE-TRE-mediated transcription. A claimed replication-competent adenovirus (Ad) vector comprises an Ad gene under transcriptional control of a CEA-TRE. Also claimed are: (1) a host cell transformed with a Ad vector as above; (2) a method of making a masked Ad, and (3) an Ad complexed with a masking agent. By providing for transcriptional initiating regulation dependent upon CEA expression, virus replication can be restricted to target cells which allow a CEA-TRE to function, particularly carcinoma cells expressing CEA. The vectors can be used to detect and monitor.
   - comprising
                                                                                                                                                                                                                                                                                                                  samples for the presence of cells that allow a CEA-TRE to function, and to selectively kill such cells, especially malignant cells. Preferred vectors contain a CEA-TRE comprising nucleotides 313-472 or 104-472 of the 472 nucleotide fragment, especially comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
             adenovirus gene under transcriptional control of carcinoembryonic antigen transcriptional regulatory element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                               This 472 nucleotide fragment comprises nucleotides -402 to +69
                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 472; DB 19; Length 472; 100.0%; Pred. No. 1.1e-127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
New adenovirus vectors, particularly for cancer therapy
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 472 BP; 142 A; 125 C; 134 G; 71 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                    enhancer and/or a promoter of the CEA gene.
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                                                                 Claim 13; Page 62-63; 95pp; English
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Matches 472; Conservative
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10654 CGIGAIGCIGAGAAGIACICCIGCCCIAGGAAGAGACICAGGGCAGAGGGAAGGACA 10713
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                                                                                                                                                                                                                                                                                    New carcinoembyronic antigen transcriptional regulatory sequence {\tt DNA} . used partic, for expressing heterologous enzymes for pro-drugs in the treatment of cancers
                                                                                                                                                                                                                                                                                                                                                              CEA genomic clone lambdacEA1 was isolated from human chromosome 19 genomic library LL19NL01 (ATCC 57766). An HindIII/Sau3A fragment of the clone extended from -10.7 to 4.6. & brelative to the start site of CEA mRNA. TRS regions of CEA are used to target e.g. cytosine deaminase to cancer cells for prodrug activation. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
                             Carcinoembryonic antigen; CEA; transcription regulatory sequence;
TRS; gene_targeting; cancer; metastasis; gene_therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.8%; Score 471; DB 16; Length 11288; 100.0%; Pred. No. 8.2e-127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11288 BP; 2940 A; 3063 C; 2953 G; 2332 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 31-37; 64pp; English.
       CEA clone HindIII-Sau3A fragment.
                                                                                                                                                              94WO-GB02546
                                                                                                                                                                                                                (WELL ) WELLCOME FOUND LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.0
nes 471; Conservative
                                                           cytosine deaminase; ss
                                                                                                                                                                                                                                          Richards CA;
                                                                                                                                                                                                                                                                  WPI; 1995-200389/26.
                                                                                       Homo sapiens
                                                                                                               WO9514100-A2
                                                                                                                                                                 L8-NOV-1994;
                                                                                                                                                                                         19-NOV-1993;
                                                                                                                                       26-MAY-1995.
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10294 AGCCACCACCAGTGAGCCTTTTTCTAGCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 10353

GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGGACCCTGCTGGG

61 10354

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121 TITCTCTGTCACAAAAGGAAAATAATCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180

GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGGAAAAAAGAGAGGAGAAAAAGA 300

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10594 GCCAGAAATGAGAGGGAGGGGACAGACACCTGAATAAAGACCACCCATGACCA 10653

GGCAGAAATGAGAGGGAGGGACAGAGGACCTGAATAAAGACCACCATGACCCA

GCAGACCAGACAGTCACAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471

421

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Recombinant nucleic acid vector; carcinoembryonic antigen; CEA; cytokine; syncytium-inducing polypeptide; fusogenic membrane glycoprotein; tumour; recombinase; tumour-specific promoter; hypoxic response element; HRB; ds; tyrosinase promoter; Cre; FLP; retroviral vector; malignant cell; cancer; cytostatic; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a recombinant nucleic acid vector comprising a first expression cassette, comprising a first promoter operably linked to a nucleic acid sequence encoding a syncytium-inducing polypeptide (such sequence recognised by a recombinase, and/or a second expression cassette comprising a tumour-specific promoter operably linked to a nucleic acid assequence encoding a recombinase. The nucleic acid of the first expression expension assette may be linked to a hypoxic response element (RRB), the second expression cassette may contain a promoter linked to a nucleic acid encoding a cytokine, and a third cassette may contain a tumour specific promoter linked to the nucleic acid encoding a cytokine, and a third cassette may contain a tumour specific promoter linked to the nucleic acid encoding the recombinase. The tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specific promoter is, for example, a carcinoembryonic antigen (CEA) promoter or a tyrosinase promoter and the recombinase is, for example, ter recombinase or FLP recombinase. The invention is useful for example, tumour size by administering the compositions as retroviral vectors, or for a cell containing the vector, to an individual in need of treatment for a disease caused by malignant cells. This sequence represents genomic DNA encoding the human carcinoembryonic antigen (CEA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant nucleic acid vector for reducing tumour size, has expression cassette comprises a promoter linked to nucleic acid sequence encoding a syncytium-inducing polypeptide and flanked on either side by
                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "Human carcinoembryonic antigen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11288 BP; 2944 A; 3060 C; 2955 G; 2329 T; 0 other;
                                                                                                                                                          Human carcinoembryonic antigen (CEA) genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bateman A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vile RG, Harrington K, Murphy S,
                                     AAS14778 standard; DNA; 11288 BP.
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                                                                                                                                                                                                                                                                                                                                                                                       10804..10938
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                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-656985/75.
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                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                      27-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-OCT-2001
                                                                              AAS14778;
                  AAS14778
                                                                                                                                                                                                                                                                                                                                                                  Key
RESULT
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New adenovirus vectors, particularly for cancer therapy - comprisi adenovirus gene under transcriptional control of carcinoembryonic antigen transcriptional regulatory element
                                                                                   Carcinoembryonic antigen; transcriptional regulatory element; CEA-TRE; human; promoter; enhancer; adenovirus; vector; cancer; gene therapy; ds.
                                                                                                                                                                                   "nucleotides -402 to +69 (Claim 13)"
                                                                Carcinoembryonic antigen gene 5' flanking region.
                                                                                                                                                                                                                                                                                                                 Schuur ER;
                                                                                                                                             Location/Qualifiers
14062..14533
           BP
                                                                                                                                                                 /*tag= a
/label= CEA-TRE
       AAV52967 standard; DNA; 15056
                                                                                                                                                                                                                                                                                                                 HG,
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                                                                                                                                                                                    /note=
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                                                                                                                                                                                                                                                                                          (CALY-) CALYDON INC
                                                                                                                                            Key
misc_feature
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                                                                                                                         Homo sapiens
                                                                                                                                                                                                    WO9839467-A2.
                                              21-DEC-1998
                                                                                                                                                                                                                                           03-MAR-1998;
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03-MAR-1997;
                                                                                                                                                                                                                       11-SEP-1998
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AAV52967
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Disclosure; Fig 2A-K; 95pp; English.

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14062 AGCCACCACCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 14121
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                                                                                                                                                                                                                                                                                                                                                                               1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTGTTG
                                                                                                                                                                                                                                                                                                                                                 Gaps
                   relative to the transcriptional start. A 472 bp fragment (see AAV52944) of this 57 flanking region (nucleotide +537 relative to the transcriptional start. A 472 bp fragment (see AAV52944) of this 57 flanking region (nucleotides -402 to +69) comprises the CEA transcriptional regulatory element (CEA-TRE) that is capable of mediating gene expression specific to cells capable of expression specific to cells capable of expression cells of CEA-TRE—mediated transcription. A dene under transcriptional control of a CEA-TRE. By providing for transcriptional initiating regulation dependent upon CEA expression, virus replication can be restricted to target cells which allow a CEA-TRE to function, particularly carcinoma cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expressing CEA. The vectors can be used to detect and monitor samples for the presence of cells that allow a CEA-TRE to function, and to selectively kill such cells, especially malignant cells.
        comprises the 5' flanking region of the
                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adenoviral vector; adenoviral gene; E3 sequence; cancer; target cell-specific transcriptional regulatory element; TRE; selective cytotoxicity; cell growth; tumour growth; ss.
                                                                                                                                                                                                                                                                                                               Length 15056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC
                                                                                                                                                                                                                                                                                 Seguence 15056 BP; 3848 A; 4125 C; 4011 G; 3072 T; 0 other;
                                                                                                                                                                                                                                                                                             99.8%; Score 471; DB 19; Length 15
100.0%; Pred. No. 9.2e-127;
...ematches 0; Indels
                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.0%; Pred. No. 9.2
Matches 471; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence of a CEA-TRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA46851 standard; DNA; 15056 BP
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The specification describes an adenoviral vector which comprises an adenoviral gene under the transcriptional control of a target cell-specific transcriptional regulatory element (TRB) and an Sequence. The vectors are useful for exerting selective cytochoxicity and/or suppressing cell growth (including tumour growth). This is and/or suppressing cell growth (including tumour growth). This is capecially useful in treating cancer in which targeted cell killing is desirable. This is also useful for targeted cytochoxic effects in other. The vectors can also be useful for detecting the cells is desirable. The vectors can also be useful for detecting the presence of cells which permit function of a target cell-specific TRE in, cfor example, an appropriate biological (such as clinical) sample. The adenovirus vector(s) can optionally selectively produce one or more proteins of interest in a target cell by using a heterologous, i.e., con-ademoviral, TRE The present sequence represents a CBA-TRE, which is used in the course of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New adenoviral vector for selective targeting of cancer cells, comprises an adenovirus gene under transcriptional control of a target cell-specific transcriptional regulatory element and an E3 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 CAGAGGICAGCACTGGGGAAGACAGGITGICCTCCCAGGGGAIGGGGGICCATCCACCIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCAGAAATGAGAGGGGAGGGGACAGGACACCTGAATAAAGACCACACCATGACCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.8%; Score 471; DB 21; Length 15056; 100.0%; Pred. No. 9.2e-127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15056 BP; 3848 A; 4125 C; 4011 G; 3072 T; 0 other;
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                                                                                                                                                                                                                                                                                Disclosure; Fig 23; 138pp; English.
                                        99WO-US31249.
                                                                    98US-0114262.
99US-0474699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 471; Conservative
                                                                                                                        (CALY-) CALYDON INC.
                                                                                                                                                                                      WPI; 2000-452409/39
                                                                                                                                                        Henderson DR,
                                           30-DEC-1999;
                                                                                          29-DEC-1999;
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           06-JUL-2000
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GGCATCATCCCACCTTCCCAGAGCCCTGGAGGATGGGGAGACCCGGGACCCTGCTGGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence comprises a transcriptional regulatory element (TRE) from a carcinoembryonic antigen gene. The TRE is used to produce an adenoviral vector of the invention. The specification under transcriptional control of a cell status specific TRE. The TRE is preferably one that is essential for adenoviral propagation. The adenovirus vectors may be used for the treatment of a range of the mounts such as lung, stomach, breast, colon and rectum, and uterine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AGCCACCACCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 ITTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAAGACCCAAGGACAGAACAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAAGAGGGACAAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                Adenovirus vectors comprising cell-status specific response elements useful in gene therapy protocols for the treatment of cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                           Carcinoembryonic antigen; adenoviral vector; adenovirus gene;
transcriptional regulatory element; TRB; transcriptional control;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 15056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15056 BP; 3848 A; 4125 C; 4011 G; 3072 T; 0 other;
                                                                                                 DNA sequence of comprising a carcinoembryonic antigen TRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.8%; Score 471; DB 21; I larity 100.0%; Pred. No. 9.2e-127; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 5A-I; 79pp; English.
                                                                                                                                                   adenoviral propagation; túmour; ss.
                      AAZ99933 standard; DNA; 15056 BP.
                                                                                                                                                                                                                                                         99WO-US20718.
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                                                                                                                                                                                                                                                                                   98US-0099791
                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                Henderson DR;
                                                                                                                                                                                                                                                                                                                     (CALY-) CALYDON INC.
                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-271456/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and cervix cancers.
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                                                                                                                                                                                                      WO200015820-A1
                                                                                                                                                                            Unidentified.
                                                                                                                                                                                                                                                       10-SEP-1999;
                                                                          25-JUL-2000
                                                                                                                                                                                                                                                                                 10-SEP-1998;
                                                                                                                                                                                                                                                                                             09-SEP-1999;
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                                                 AAZ99933;
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                                                                                                                                                                                                                                                                                                                                              DC,
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RESULT 6
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CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAAGGACA 420
GGCAGAAATGAGAGGGGAGGGACGGACAGACACCTGAATAAAGACCACACCATGACCA 360
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                                                                                                                                                                                                                                                      Adenovirus; ADP; replication-competent; adenoviral vector; TRE; PCR; transcriptional regulatory element; mutation; deletion; IRES; primer; promoter; internal ribosome entry site; cytotoxic; cancer; bladder; amplify; polymerase châin reaction; alpha-fetoprotein; AFP; EMCV; encephalomycarditis virus; vascular endothelial growth factor; VEGF; immunoglobulin heavy-chain binding protein; BiP; uroplakin II; PDGF; platelet derived growth factor; hypoxia responsive element; HRE; prostate-specific antigen; PSA; ss.
                                                                                                  GCAGACCAGACAGTCACAGCAGCCTTGACAAACGTTCCTGGAACTCAAGC 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Replication-competent adenoviral vector, useful e.g. for killing cells, contains two genes linked by internal ribosome entry site controlled by target-specific regulator
                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/note= "Transcription start site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example; Page 117-125; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                      BP.
                                                                                                                                                                AAH43620 standard; cDNA; 15056
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                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                             precursor_RNA
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301
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                                                                                                                                            RESULT 7
AAH43620
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The sequences given in AAH43607-22 represent sequences which may used in the replication-competent adenoviral vector (A) of the invention. The vector contains two genes (G1, G2) that are co-transcribed as a single mRNA and under control of a heterologous, target cell-specific transcriptional regulatory element (TRE). G2 has a mutation in, or deletion of, its endogenous promoter and is controlled from an internal ribosome entry site (IRES). (A) has greater specificity for a target cell than a similar vector in which TRE is operably linked to a gene and which lacks an IRES. (A) are used to modify the genotype of target cells, optionally in vitro with subsequent return of altered cells to the host and where G2 is a cytotoxic gene, to confer selective cytotoxicity to target cells, especially for killing cancer cells. Also to all a recommend to the confer selective cytotoxicity to target cells, especially for killing cancer cells. Also

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(CALY-) CALYDON INC
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ID ABK9
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cancer cells. The target cell-specific TRE ensures that (A) has better targeting specificity, with minimal replication in non-target cells, so a runaway infection is prevented but production of adenoviral proteins in target cells activates and/or stimulates the immune response against target cells producing such proteins. The use of an IRES (rather than two identical control elements) eliminates the risk of homologous recombination and may provide enough extra space for an additional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumour growth suppression; adenovirus vector; antineoplastic agent; transcriptional regulatory element; TRE; radiotherapy; bladder cancer; prostate cancer; liver cancer; breast cancer; colon cancer; melanoma; ovarian cancer; pancreatic cancer; lung cancer; brain cancer; therapy;
                                                                                                                                                                                                               GCCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGCTGGG
                                                                                                                                                                                                                                           121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG
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                                                                                                                                                                                                   GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGGAGACCCGGGACCCTGCTGGG
                                                                                                                                        Gaps
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0
                                                                                                                  Score 471; DB 22; Length 15056; Pred. No. 9.2e-127;
                                                                                              Sequence 15056 BP; 3848 A; 4125 C; 4011 G; 3072 T; 0 other;
                                                                                                                                        Indels
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                                                                                                            99.8%; Stc...
v 100.0%; Pred. No. ...
no. 0; Mismatches
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                                                                                                                                          Conservative
                                                                                                                               Similarity
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                                                                                                                                         471;
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                                                                                                                       Query Match
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                                                                                                                                                                                                         This sequence represents a CEA-TRE fusion protein coding sequence used in the scope of the invention. The invention relates to a method for the suppression of tumour growth comprising the administration of:

(a) a target cell-specific adenovirus vector comprising an adenoviral gene essential for replication under transcriptional control of a target cell-specific transcriptional requisition and adenovirus where the amount of (a) and/or (b) at least one antineoplastic agent; or (c) a course of radiotherapy where the amount of (a) and/or (b) or (c) is lower than that known to be effective for suppressing tumour growth when administered alone. For suppression of tumour growth for treatment of e.g. bladder cancer, prostate cancer, liver cancer, breast cancer, colon cancer, melanoma, ovarian cancer, liver cancer, lung cancer colon cancer. The combinations enhance the efficacy of treatment, allowing lower doses to be administered, reducing toxicity and suffering of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. m.:
                                                                                                                                                                         Claim 12; Page 185-193; 248pp; English.
                                                                                                                               antineoplastic agent or radiotherapy
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Chen Y, Henderson DR;
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Matches 471; Conservative
                                           WPI; 2001-648426/74
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Disclosure, Fig. 6; 64pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CEA genomic clone.
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01-NOV-1995
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an adenovirus vector (AV) comprising an AV gene under transcriptional control of a cell type-specific transcriptional regulatory element (TRE) and optionally a first AV gene under control of a first cell type-specific TRE and a second gene under control of second cell type-specific TRE, where the first and second cell type-specific TRE, where the first and second cell type-specific TREs are substantially identical. When the vector is introduced into a cell (e.g. prostate cell, liver cell, breast cancer cell or colon cancer cell) it allows the cell type-specific TRE to function, resulting in cytotoxicity. The vector is useful for suppressing used in the scope of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCGAAAAGATTIGTCTGAGGAACTGAAAATAGAAGGGAAAAAAAGAGGAGGGACAAAAGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCAGAAATGAGAGGGAGGGGACAGAGGACACCTGAATAAAGACCACCATGACCCA 360
                                                                                                            Adenovirus; transcriptional regulatory element; TRE; prostate; liver; breast cancer; colon cancer; antitumour; gene; ds; probasin; PB; human; rat; carcinoembryonic antigen; prostate-specific antigen; ADP; adenovirus death protein; glandular kallikrein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel adenovirus vector comprises adenovirus gene under transcriptional control of cell-type specific transcriptional response element for conferring selective toxicity on target cell and for suppressing tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AGCCACCACCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GCCATCATCCCACCTTCCCAGAGCCCTGGAGGGATGGGGGAGACCCGGGACCCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 IITCTCTGTCACAAAAGGAAAATAATCCCCCTGGTGTGACAGAACCCAAGGACAGAAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prostate-specific antigen transcriptional regulatory elelment (TRE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15056 BP; 3848 A; 4125 C; 4011 G; 3072 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 471; DB 24; I
Pred. No. 9.2e-127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 15; 83pp; English.
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100.0%;
                                                                                                                                                                                                                                                                                                                                                06-DEC-2000; 2000US-0732169.
                                                                                                                                                                                                                                                                                                                                                                                                98US-0151376.
                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           HENDERSON D R.
                                                                                                                                                                                                                                                                                                                                                                                                                                      (HEND/) HENDERSON D
(SCHU/) SCHUUR E R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-582468/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                               US2002068049-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Henderson DR,
                                                                                                                                                                                                                                                                                                                                                                                                10-SEP-1998;
                                                                                                                                                                                                                                                                                                        06-JUN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New carcinoembyronic antigen transcriptional regulatory sequence DNA used partic, for expressing heterologous enzymes for pro-drugs in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AGCCACCACCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGGATGGGGAACCCGGGACCCTGGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CEA genomic clone lambdacEA1 was isolated from human chromosome 19 genomic library LL19NL01 (ATCC 57766). HindIII/Sau3A and HindIII fragments of the clone were sequenced and combined to obtain the sequence given in AAQ90511, which extends from -14.4 to +0.6 kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carcinoembryonic antigen; CEA; transcription regulatory sequence; TRS; gene targeting; cancer; metastasis; gene therapy; cytosine deaminase; hybridization; probe; ss.
                                                                                                                                                       421 GCAGACCAGACAGTCACAGCGTTGACAAAACGTTCCTGGAACTCAAGC 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 14556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14556 BP; 3721 A; 3995 C; 3874 G; 2966 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.1%; Score 359; DB 16; 96.9%; Pred. No. 4.3e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            relative to the start site of CEA mRNA. (Updated on 25-MAR-2003 to correct PN field.)
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                                             301 GGCAGAAATGAGAGGGGAGGGGACAGAGACACCTGAATAAAGACCACACACCATGACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cloning carcinoembryonic antigen promoter DNA - used for tumour gene
                                                                                                                                                                                                                                                                                                                                                                           Carcinoembryonic antigen; CEA; promoter; colon cancer; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel DNA sequence which is dissimilar f the carcinoembryonic antigen (CEA) promoter of colon cancer. In CEA secretary tumour gene therapy, the gene segment is recombined with therapeutic gene, so that killing of tumour cells may be effected selectively while keeping normal cells unaffected. This sequence represents promoter used to describe the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.7%; Score 225; DB 20; Length 271; 100.0%; Pred. No. 1.1e-55;
                                                                                                                                                                                                       14000 GCAGACCAGACAGTCACAGCCTTGACAAAACGTT 14036
                                                                                                                                                                                           457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 271 BP; 100 A; 57 C; 82 G; 32 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SCRE-) SCI RES & TRAINING SECTION MEDICAL MATTE.
                                                                                                                                                                                           GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTT
                                                                                                                                                                                                                                                                                                                                                    Carcinoembryonic antigen homologue promoter.
                                                                                                                                                                                                                                                                                                                                                                                       tumour; secretion; tumour cell; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 3; 10pp; Chinese.
                                                                                                                                                                                                                                                                           AAZ09584 standard; DNA; 271 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97CN-0114280
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                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-431041/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jiang Y, Wang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-0CT-1997;
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                                                                                                                                                                                                                                                                                                    AAZ09584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3;
                                               241
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181
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The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (GS) identified by CC (GCA), by detecting the level of expression of gene(s) (GS) identified by the analysis as given in the specification, and comparing the expression level to an expression level in an unactivated (GC, where differential expression of GS is indicative of GCA.

CC Also included are modulating (MZ) GA by contacting GC with an agent that alters the expression of at least one gene in GS; (2) screening (M3) correcting of an agent capable of modulating GCA or an inflammation (especially Chronic) in a tissue, an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the correction of a tissue, an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the cubic expression in a sample of the tissue of gene(s) from GS, where the level of expression of the gene is indicative of inflammation.

CC (H) treating (MS) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen

CC (A) treating (MS) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen

CC or sterile inflammatory disease, by contacting a tissue having
AATGAGAGGGGAGAGAGAGACACCTGAATAAAGACCACACACCCATGACCCACGGGT 366
                                                                               Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rhemmatoid arthritis; glomerulonephritis; asthma; thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cDNA differentially expressed in granulocytic cells #33
                                                                                                                                                                                             CAGACAGICACAGCGITGACAAACGITCCIGGAACICAAGC 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vockley J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamaga S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID No 33; 114pp; English.
                                                                                                                                                                                                                                                                                                                    ВP
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                                                                                                                                                                                                                                                                                                                 ABK83462 standard; cDNA; 39801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-OCT-2001; 2001WO-US30821.
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                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-2002
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                                                 61
                                                                                                                                                                            427
                                                                                                                                                                                                                                                                                                                                                               ABK83462;
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                                                                                                                                                                                                                                                                                 RESULT 12
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Homo sapiens.
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inflammation with an agent that modulates the expression of gene(s)
from Gs in the tissue. MI is useful for detecting GCA: M2 is useful for
modulating GA: M3 is useful for screening an agent capable of modulating
GCA preferably in an inflammation in a tissue; M4 is useful for
GCA preferably in an inflammation in a tissue; M4 is useful for
cresponse in a subject, exposure of a subject to a pathogen or sterile
cresponse in a subject, exposure of a subject to a pathogen or sterile
cresponse in a subject, troops in the material inflammatory datases (e.g. postiasis, rheumatoid arthritis,
domerulonephitis, asthma, thrombosis, cardiac reperfusion injury, renal
creperfusion injury, ARDS, adult respiratory distress syndrome,
inflammatory Dowel disease, Crohn's disease, ulcerative colitis,
periodontal disease; also bacterial infection, viral infection,
periodontal disease; also bacterial infection, viral infection,
creful for treating one of the above conditions. The present
creful for treating one of the above conditions. The present
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creful from part of this parent did not form part
creful format directly from MPDO at the condition of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                    37496 GGAAACAGITCCCCAAGITTGGGAAGACCCCAGAGITACTGTTTGTGGTGACATTCCCA 37437
                                                                                                                                                                                                                                                                                                                                                                                                    37557
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                                                                                                                                                                                                                                                                                                                                                                                                                    78 CCAGAGCCCTGGAGAGGATGGGGAGACC-CGGGACCCTGCTGGGTTTCTCTGTCACAAAG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182
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                                                                                                                                                                                                                                                                                                                                                             18 CCITITICIAGCCCCCAGAGCCACCICIGICACCIICCTGIIGGGCAICAICCCACCIIC
                                                                                                                                                                                                                                                                                                                                                                            137 GAAAATAATCCCCCTGGTGTGACAGACCCAAGGACA--------GAACACAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 GCCGAAAAGAITIGTCTGAGGA----ACTGAAAAIAGAAGGGAAAAAAG-AGGAGGGA
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carcinoembryonic antigen; CEA; transcription regulatory sequence; TRS; gene targeting; cancer; metastasis; gene therapy;
                                                                                                                                                                                                                                                                                                             DB 24; Length 39801;
                                                                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                                                                                                                                          Sequence 39801 BP; 9969 A; 9367 C; 9531 G; 10934 T; 0 other;
                                                                                                                                                                                                                                                                                                     / Match 25.6%; Score 120.8; DB 24; Length Local Similarity 66.1%; Pred. No. 2.1e-24; nes 292; Conservative 0; Mismatches 122; Indels
                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ73990 standard; DNA; 3774 BP
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01-NOV-1995
                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                               Matches
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1837
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                                                                                                                                                                                                                                   for expressing heterologous enzymes for pro-drugs in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 CACCACCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1778 CTGCATCACAAAGAAAATAATCCCCCAGGTTCGGATTCCCAGGGCTCTGTATGTGGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 GACAGACCCAAGGACAGAACACCAGGAGGTCAGCACTGGGGAAGACAGGGTTGTCCTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 ATCAICCCACCTTCCCAGAGCCCTGGAGAGCATGGGGGAGACCCGGGACCCTGCTGGGGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L9-----
                                                                                                                                                                                                             New carcinoembyronic antigen transcriptional regulatory sequence DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                              CEA genomic clone lambdaCEA1 was isolated from human chromosome 19 genomic library LL19NL01 (ATCC 57766). An HindlII fragment of the clone extended from -14.5 to -10.7 kb relative to the start site of CEA mRNA. TRS regions of CEA are used to target e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cDNA differentially expressed in granulocytic cells #33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel diseas crohn's disease; ulcerative colitis; periodontal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ss; granulocytic cell; DNA chip; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                   cytosine deaminase to cancer cells for prodrug activation. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 94; DB 16; Length 377
Pred. No. 5.2e-17;
n. Wigmatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3774 BP; 906 A; 1066 C; 1057 G; 745 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 CICTGTCACAAAGGAAAATAATCCCCCTGGT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1898 AGGGACAGGGTGCACCATGC 1923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217 AGGGGATGGGGGTCCATCCACCTTGC 242
                                                                                                                                                                                                                                                                                       Disclosure; Page 37-39; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABK83462 standard; cDNA; 39801 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.9%;
69.5%;
      94WO-GB02546
                                                93US-0154712
                                                                                     (WELL ) WELLCOME FOUND LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 69.5
ses 185; Conservative
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                                                                                                                              Huber B, Richards CA;
                                                                                                                                                                                                                                used partic. for expu
treatment of cancers
                                                                                                                                                                        WPI; 1995-200389/26.
18-NOV-1994;
                                           19-NOV-1993;
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326

368

--CACCCATGACCCACGTGATGC

9335 TAAGGGATGGGGGTCCCAATAAGCCTTGCTTCTCACAGCGTGTGTAAGGAACTGAAATG 9394

270 ---ATAGAAGGGAAAAAAGAGGGACCAGAAAGAGGCAGAAATGAGAGGGGAGGGGACAG

δy pp

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The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (GS) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated controlled are modulating (M2) GA by contacting GC with an agent Also included are modulating (M2) GA by contacting GCA with an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a current of a pathogen or sterile inflammatory disease using the corporation of a thermal contact of a subject or a pathogen or sterile inflammatory disease, by detecting the chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation (disease, by detecting the contacting (M5) an inflammation of the gene (S) from GS, where the level of expression of the gene is indicative of inflammation; an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation (despecially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation (despecially chronic) or in a tissue, an allergic response that modulates the expression of gene(s) from GS, where the inflammatory disease, by contacting a tissue having contacting GA; M3 is useful for screening an agent capable of modulating GA; M3 is useful for screening an agent particle of a subject of a pathogen or sterile inflammation in a tissue; M4 is useful for screening or sparile or screening an agent particle of a subject to a pathogen or sterile or screening an agent particle of a subject or sparile or screening an agent particle of a subject or an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation with an inflammation in a tissue; M4 is useful for screening or sterile or sparile or screening an agent to a subject to a pathogen or screening an allergic response in a subject t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, ARDS, adult respiratory distress syndrome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease, also bacterial infection, viral infection, parastic infection, protezoal infection, imagal infection and M5 is sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIDO at from wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 39801 BP; 9969 A; 9367 C; 9531 G; 10934 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                 Vockley J;
granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                 Yamaga S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID No 33; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    Weissman SM,
                                                                                                                                                                                                                               03-OCT-2001; 2001WO-US30821.
                                                                                                                                                                                                                                                                                       03-0CT-2000; 2000US-237189P.
                                                                                                                                                                                                                                                                                                                                            (GENE-) GENE LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-435328/46.
                                                                                                                                                                                                                                                                                                                                                                                                    Beazer-Barclay Y,
                                                                                                               WO200228999-A2
                                                             Homo sapiens.
                                                                                                                                                                       11-APR-2002
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9455 AAAGGCIACCIGIGCAGAICCICATIGCCACTIACCITTCCCCGCCCCCACCCTGGCCC 9514
                                                                                                                                                                                     The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as
                                                                                                                                      drug toxicity, drug efficacy and drug metabolism. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          markers that can be used to monitor disease states, disease progression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene: liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diagnosing and detecting the progression of liver cancer, hepatcocallular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vockley JG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene #2317 used to diagnose liver cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 2317; 298pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peres-Da-Silva S,
                                                                                                                                                                                                                                                                                                                                               9575 GACAGTCACAGTAGCTCTGACAAGA 9599
                                                                                                                                                                                                                                                                                                        453
                                                                                                                                                                                                                                                                                                        GACAGTCACAGCAGCCTTGACAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABN95819 standard; DNA; 2974 BP
327 AGGACACCTGAATAAAGACCA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-OCT-2001; 2001WO-US30589.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-OCT-2000; 2000US-237054P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L3-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABN95819;
                                                                                                                                                                                                                                                                                                               429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
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Score 85.8; DB 24; Length 39801; Pred. No. 3.4e-14; 0; Mismatches 97; Indels 27;

18.2%; 61.8%;

Matches 201; Conservative

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Local Similarity

Query Match

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September 26, 2003, 12:22:31; Search time 71 Seconds (without alignments) 2934.265 Million cell updates/sec
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472
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Gaps

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100.0%; Score 472; DB 4; Length 472; 100.0%; Pred. No. 6.3e-129; arive 0; Mismatches 0; Indels

Query Match Best Local Similarity 100.0 Matches 472; Conservative

	JS-09-184-418C-29 Segmence 29 April	,	Sequence 3, Appli	US-07-891-942G-11 Segmence 11, april	121	'TOT acrombac .	US-US-UN-UND-32 Sequence 32, Appl	Segmence 32.	1	Sequence 3,	sednence 3,	00 000-455-3 Sequence 3, Appli	US-08-744-231-3 Sequence 3 April	US-08-916-421B-1 Segment 1 Prof. 1	, contact T	sedneuce 3,	Sequence 3,	_	'* Something *'	, sequence 1,	-09-203-28 Sequence 28, Appl	-2 Seguence 2.	ì.	יין אַרייין די	SENGMNOTIV	CTURRENTS	
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c	97	53	UK	0 1	3.1	32	0.0	00	34	32	36	27	~ 1	986	39	40	7	4.4	42	4	7 7		C 45				

APPLICANT: Henderson, Daniel R. APPLICANT: Henderson, Daniel R. TTLE OF INVENTION: De Chao TITLE OF INVENTION: ADBROVYRUS VECTORS of TITLE OF INVENTION: OF USING SAME NUMBER OF SEQUENCES: 41 CORRESPONDENCES: 41 CORRESPONDENCE ADDRESS: ADDRESSEE: MORRISON & POERSTER STREET: 755 PAGE MILL ROAD CITY: Palo Alto STREET: 755 PAGE MILL ROAD CITY: Palo Alto STREET: 155 PAGE MILL ROAD CITY: Palo Alto STREET: DAS ADDRESSEE: OWNUTER: USA COUNTER: USA COUNTER: USA COUNTER: IBM COMPATION: WINDOWS SOFTWARE: PASSERO (FOR WINDOWS SOFTWARE: PASSERO (FOR WINDOWS SOFTWARE: PASSERO (FOR WINDOWS SOFTWARE: PAPLICATION DATA: APPLICATION NUMBER: US/09/033,556 FILING DATE: REDERENCE/DOCKET NUMBER: 34802-20010.05 REFERENCE/DOCKET NUMBER: 34802-20010.05 TELECOMMUNICATION INFORMATION: TELEPHONE: 650-494-0792 TELERAX: 706141 INFORMATION FOR SEQ. ID NO: 7:	Sequence 7, Application US/09033556 Patent No. 6422700 GENERAL INFORMATION: APPLICANT: Henderson, Daniel R. APPLICANT: Yu, De Chao APPLICANT: Yu, De Chao APPLICANT: Yu, De Chao TITLE OF INVENTION: HETEROLOGOUS TRANSCRIPTION REGULATORY TITLE OF INVENTION: OF USING SAME ADDRESSEE: MORESS: ADDRESSEE: MORESS: ADDRESSEE: MORESON & FOERSTER STREET: 755 PAGE MILL ROAD CITY: Palo Alto STRATE: CA COUNTRY: USA ZIP: 94304-1018 COMPUTER: EBM Compatible OPERATING SYSTEM: Windows Version 2.0b CURRENT APPLICATION DATA: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: Windows SOFTWARE: ESSESSE OF WINDOWS SOFTWARE: ESSESSE OF WINDOWS SOFTWARE: PROBLECATION DATA: REDILCATION UNBER: US/09/033,556 CLASSIFICATION DATA: APPLICATION NUMBER: 34802-20010.00 TELECOMMUNICATION NUMBER: 34802-20010.00 TELECOMMUNICATION INPERMINENT APPLICATION NUMBER: 34802-20010.00 TELECOMMUNICATION INPERMINENT APPLICATION NUMBER: 34802-20010.00 TELECOMMUNICATION NUMBER: 34802-20010.00 TELECOMMUNICATION NUMBER: A0,130 REPERRENCE/DOCKET NUMBER: 34802-20010.00 TELEDRIONE: 650-813-5600 TELECOMMUNICATION NUMBER: A0,130 REPERRENCE/DOCKET NUMBER: 34802-20010.00 TELEDRIONE: 650-813-5600 TELEDRIONE: 650-813-5600 TELEDRIONE: 650-813-5600 TELEDRIONE FOR EACH OF 72	ELEMENTS AND METHODS	THODS
SEQUENCE CHARACTERISTICS: LENGTH: 472 base pairs			
TYPE: nucleic acid STRANDEDNESS: single			

QY	QY 241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGGACAAAAGA 300 DD 10534 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAGAGGGACAAAAGA 10593 QY 301 GGCAGAAATGAGGGGAGGGACAGAGGACCCTGAATAAAGACCACCCCATGACCA BD 10594 GGCAGAAATGAGGGGACAGAGGACACCTGAATAAAGACCACCCCATGACCA CQY 361 CGTGATGCTGAGAGGACAGACGACACCTGAGGACACACCCCATGACCA QY 361 CGTGATGCTGAAAGATACCTGCCTGCGAGGAAGAGACACACCCCATGACCA DD 10554 GCTGATGCTGAAAGATACTCTGCCTGCGTAGGAAGAGACACACAC
241 GCCGAAAGGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGA 301 GGCAGAAATGAGGGGACAGGGACAGGGACAAAAGA 301 GGCAGAAATGAGGGGACAGGGGACAGGACCCTGAATAAAGACCCACCC	RESULT 3 US-00-481-968A-4 Sequence 4, Application US/08481968A Sequence 4, Application US/08481968A Patent No. 6300400. GENERAL INFORMATION: APPLICANT: Huber, Brian APPLICANT: Richards, Cynthia TITLE OF INVENTION: Molecular Constructs Comprising a Carcinoembryonic Antigen TITLE OF INVENTION: Transcriptional Regulatory Region FILE REPERENCE: PB1087084
OY 421 GCAGACCAGACAGCCTGACAAAAGGTTCCTGGAACTCAAGCA 472	DIA DIA
GENERAL INFORMATION: APPLICANT: Richards, Cynthia Ann APPLICANT: Richards, Cynthia Ann APPLICANT: Huber, Brian E. TITLE OF INVENTION: Transcriptional Regulatory Sequence of Carcinoembryonic Partent No. 6194211 TITLE OF INVENTION: Antiqen for Expression Targeting FILE REFERENCE: PB1508U5W CURRENT APPLICATION NUMBER: US/08/646,301A CURRENT APPLICATION NUMBER: US/08/646,301A SUFFMENT FILING DATE: 1996-05-16 NUMBER OF SEQ ID NOS: 25 SOFFWARE: Patentin Ver. 2.1 SEQ ID NO 1	Ouery Match 99.8%; Score 471; DB 4; Length 11288; Best Local Similarity 100.0%; Pred. No. 4.4e-128; Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 AGCCACCACGAGAGCCTTTTCTAGCCCCAGAGCCACTCTGTCACTTCTGTG 60
, p	121
Query Match 99.8%; Score 471; DB 3; Length 11288; Best Local Similarity 100.0%; Pred. No. 4.4e-128; Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY 181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCACCTT 240
OY 1 AGCCACCACCAGGAGCCTTTTTCTAGCCCCAGAGCCACCTGGTCACCTTCTGTTG 60	OY 241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGGGGGGGG
QY 61 GGGATCATCCCACATCCCACAGCCCTGGAGAGCATGGGGACCCGGGACCCTGCTGGG 120 Db 10354 GGCATCATCCCAGAGCCTTGGAGAGCATGGGGAGACCGGGGACCCTGCTGGG 10413	OY 301 GGCAGAAATGAGGGGACGGACAGGACACCTGAATAAAGACCACCACCCATGACCCA 360
OY 121 TITCICIGCACAAAGGAAAATAATCCCCTGGTGACAGACCAAGGACAGAACACAG 180	OY 361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGGAGGAGGAGGAACACA 420
0y 181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCACCTT 240	OY 421 GCACACACACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471

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14182 ITTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAACCAAGGACAGAAGAAG 14241
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APPLICANT: Richards, Cynthia Ann
APPLICANT: Huber, Brian E.
TITLE OF INVENTION: Iranscriptional Regulatory Sequence of Carcinoembryonic
Patent No. 6194211
TITLE OF INVENTION: Antigen for Expression Targeting
FILE REFERENCE: PB1508USW
CURRENT APPLICATION NUMBER: US/08/646,301A
CURRENT FILING DATE: 1996-05-16
                                                                                                                                                                                                                           61 GGCATCATCCTACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGGACCCTGCTGGG 120
                                                                                                                                                                                                                                                                                 121 ITTCTCIGTCACAAAAGGAAAATAATCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
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                                                                                                                                                                                                                                          241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAAGGGGACAGAAAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 GCCAGAAAIGAGAGGGAGGGGCACAGAGGACACCTGAAIAAAGACCACACCCAIGACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGAGGAAGAAGACA
                                                                                                                                                    Gaps
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                                                                                                               99.8%; Score 471; DB 4; Length 15056; ilarity 100.0%; Pred. No. 5e-128; Conservative 0; Mismatches 0; Indels 0
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NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08646301A
Patent No. 6194211
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Best Local Similarity 69.5
Matches 185; Conservative
                                                    TYPE: DNA
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ve
                                                                                                                              Similarity
                           SEQ ID NO 10
LENGTH: 15056
                                                                                  US-09-474-699-10
                                                                                                                       Best Local Sim
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                                                                GENERAL INFORMATION:
APPLICANT: Huber, Brian
APPLICANT: Richards, Cynthia
TITLE OF INVENTION: Molecular Constructs Containing a Carcinoembryonic Antigen Regu
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                                                                                                                                                                                                                                                                                                       Length 11288;
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APPLICANT: Henderson, Daniel R.
APPLICANT: Yu, De Chao
TITLE OF INVENTION: TARGET CELL-SPECIFIC ADENOVIRAL VECTORS
TITLE OF INVENTION: CONTAINING E3 AND METHODS OF USE IHEREOF
FILE REFREEMENT 348022001300
CURRENT APPLICATION NUMBER: 02/09/474,699
CURRENT FILING DAFE: 1999-12-29
PRIOR APPLICATION NUMBER: 60/114,262
PRIOR PLILING DATE: 1998-12-30
                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                     Pred. No. 4.4e-128;
                                                                                                                                                                                                                                                                                                 99.8%; Score 471; DB 4;
100.0%; Pred. No. 4.4e-12
cive 0; Mismatches 0
                                                                                                                                                    CURRENT APPLICATION UNMER: US/08/154,7128
CURRENT FILING DATE: 1993-11-19
NUMBER OF SEQ ID NOS: 36
                                          Sequence 4, Application US/08154712B
Patent No. 6337209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/09474699 Patent No. 6495130
                                                                                                                                                                                                PatentIn version 3.0
                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.1
Matches 471; Conservative
                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                            LENGTH: 11288
                          US-08-154-712B-4
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US-09-474-699-10
                                                                                                                                                                                                            SEQ ID NO 4
                                                                                                                                                                                                                                          TYPE: DNA
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Best Local
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1662 CAGTARARCAGTGAGCTCCTATCCAGCCCCCAGAGCCACCTCTGTCACCTTGTGGC 1721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 GACAGACCCAAGGACAGAACACAGCAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCC
                                                                                                                                                                               Score 94; DB 4; Length 3774;
Pred. No. 6.7e-18;
                                                                                                                                                                                                6.7e-18;
ches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                   124 CICIGICACAAAGGAAAAIAAICCCCCTGGI-
CURRENT APPLICATION NUMBER: US/08/154,712B
CURRENT FILING DATE: 1993-11-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1898 AGGGGACAGGGGTGCACCAGCCTTGC 1923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 AGGGGATGGGGGTCCATCCACCTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/08232463 Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 304 TELECOMMUNICATION INFORMATION:
                                          NOS: 36
PatentIn version 3.0
                                                                                                                                                                                   19.9%;
69.5%;
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(703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                     al Similarity 69.5
185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-154-712B-5
                                         ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5670367
GENERAL INFORMATION:
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                                         NUMBER OF SEQ
                                                                                             3774
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                                                         SOFTWARE:
SEQ ID NO 5
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Matches
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Patent No. 6337209
GENERAL INFORMATION:
APPLICANT: Huber, Brian
APPLICANT: Richards, Cynthia
TITLE OF INVENTION: Molecular Constructs Containing a Carcincembryonic Antigen Reguring Reference: PB1087053
                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08481968A

Patent No. 630490

Patent No. 630490

PAPLICANT: Huber, Brian

APPLICANT: Richards, Cynthia

APPLICAN: Richards, Cynthia

APPLICAN: Molecular Constructs Comprising a Carcinoembryonic Antigen (CEM

TITLE OF INVENTION: Transcriptional Regulatory Region
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                                                                                                                                                                                        1662 CAGIAAACAGIGAGCICCIAICCAGCCCCCAGAGCCACCICIGICACCIICCIGCIGGGC 1721
                                          216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 ATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGGACCCTGCTGCTGGTTT 123
                                                                                               ---GT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 CACCACCCAGIGAGCCITTITCIAGCCCCCAGAGCCACCICIGICACCITCCIGIIGGGC
                          ATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGGTTT
                                                                                                                                  1778 CIGCATCACAAAAAAAAAAATAATCCCCCAGGTTCGGATTCCCCAGGGCTCTGTATGTGGAGCT
                                                                                                                                                                       GACAGACCCAAGGACAGAACACAGCAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CICIGICACAAAGGAAAITAAICCCCCTGGI
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                                                                                                CICTGICACAAAGGAAAAIAAICCCCCIGGI
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                                                                                                                                                                                                                                            217 AGGGGATGGGGGTCCATCCACCTTGC 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 69.5%;
Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PB1087US4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
US-08-154-712B-5
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                                                                                                                                                                                                                                                                                                                         76 ICCCAGAGCCCIGGAGGAIGGGGAGACCCGGGACCCIGCIGGGTITCICTGTCACAAA 135
                                                                                                                                                                                                                                                                                                  136 GGAAAATAATCCCCCTGGTGTGACAACCCAAGGACAGAACACAGCAGAGGTCAGCACTG 195
                                                                                                                                                                                                                                                                                                                                                               316 GGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCAACGTGATGCTGAGAAG 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       256 CTGAGGAACTGAAAATAGAAGGGAAAAAAGGGAGGGACAAAAAGAGGCAGAAATGAGAG
                                                                                                                                                                               DB 1; Length 7218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Reed, Steven G.
APPLICANT: Reed, Michael J.
APPLICANT: Hooles, Michael J.
APPLICANT: Mochameth, Roadoh
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.475c1
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: US/09/370,838
EARLIER APPLICATION NUMBER: US/09/285,323
EARLIER APPLICATION NUMBER: US/09/285,323
EARLIER FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 387;
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                                                                                                                                                                     Query Match 15.1%; Score 71.2; DB 1; Best Local Similarity 4.0%; Pred. No. 4.1e-11; Matches 16; Conservative 236; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      436 ACAGCAGCCTTGACAAACGTTCCTGGAACTCAAGC 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.2%; Score 57.6; DB 4; 93.8%; Pred. No. 1.2e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 177, Application US/09370838 Patent No. 6444425
              INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
                                              LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 12.28
Best Local Similarity 93.88
Matches 60; Conservative
                                                                                                                       US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapien
                                                                                           TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-370-838-177
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TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: C. MOILOW et al.
TITLE OF INVENTION: ENCAPSIDAIED RECOMBINANT VIRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.4%; Score 54; DB 1; LA 100.0%; Pred. No. 2.8e-06; vative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                   E: LAHIVE & COCKFIELD
60 STATE STREET, SULTE 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/389,459A
FILING DATE: 15 FEB-1995
                                                                                                                                                             Sequence 16, Application US/08389459A
Patent No. 5817512
GENERAL INFORMATION:
APPLICANT: MOTICOW, Casey D. and Port
ITILE OF INVENTION: ENCAPSIDATED REC
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/087,009
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-987-867A-16; Sequence 16, Application US/08987867A; Patent No. 6063384; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Silveri, Jean M.
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: UA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGIH: 2220 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54; Conservative
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ADDRESSEE: LAHIVE & (
                                                                                                                                                                                                                                                                                                                                                                  MASSACHUSETTS
USA
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
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Best Local Similarity
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                                                   468 AAGC 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 15 CLASSIFICATION:
                                                                                  AAGC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                 BOSTON
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                   02109
                                                                                                                               RESULT 11
US-08-389-459A-16
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US-08-389-459A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                  29
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STATE:
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us-10-045-116-1.rni

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320 GGGACAGGACACCTGAATAAAGAC 345
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
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229 RGRCRGRURARARCRURCRURURGRC 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/09244796; Patent No. 6281344; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/09007005B Patent No. 6258558 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LCCATION: (1)...(289)
COTHER INFORMATION: n = A,T,C or G
US-09-007-005-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: RNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SZOSTAK, Jack W. APPLICANT: Roberts, Richard W. APPLICANT: Liu, Rihe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 8.3%
Best Local Similarity 3.9%,
Matches 8; Conservative
                                                                                                                                                                                                                                      249 AGCCCAAGC 241
                                                                                                                                                                                                   463 AACTCAAGC 471
US-09-385-982-486
                                                                                                                                                                                                                                                                                                    RESULT 14
US-09-007-005-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       419 CAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA
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GENERAL INFORMATION:

APPLICANT: ENDEGE, WILSON O., ET AL.

APPLICANT: ENDEGE, WILSON O., ET AL.

TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

TITLE OF INVENTION: PRODUCTS: II

FILE REFERENCE: CCDNA-260XX

CURRENT APPLICATION NUMBER: 09/328,111

EARLIER APPLICATION NUMBER: 09/328,111

EARLIER PILING DATE: 1999-06-08

EARLIER FILING DATE: 1999-01-27

EARLIER FILING DATE: 1999-01-27

EARLIER PILING DATE: 1998-01-27

EARLIER FILING DATE: 1998-01-27

EARLIER FILING DATE: 1998-01-27

EARLIER FILING DATE: 1998-08-31

NUMBER OF SEQ ID NOS: 544

NUMBER OF SEQ ID NOS: 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2220;
      INVENTION: NUCLEIC ACID AND METHODS OF MAKING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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11.4%; Score 54; DB 3; L
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 54; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/987,867A
FILING DATE: 09 DEC-1997
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/087,009
FILING DATE: 01-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UAP-004CPDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 486, Application US/09385982; Patent No. 6262334
                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: UAP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 16:
                                                                                     E: LAHIVE & COCKFIELD
28 STATE STREET
                               USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2220 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                           STREET: 28 STATE STRE CITY: BOSTON STATE: MASSACHUSETTS
            TITLE OF INVENTION: NUC
TITLE OF INVENTION: USI
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
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US-09-385-982-486/c
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US-08-987-867A-16
                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                            SOFTWARE:
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LENGTH: 319
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                                                                                                                                   404 CAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAAC-GTTCCTGG
                                                    Gaps
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Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN TITLE OF INVENTION: FUSIONS FILE REPRESENCE: 00786/350003 CURRENT APPLICATION NUMBER: US/09/007,005B CURRENT APPLICATION NUMBER: 00/035,963 EARLIER PRING DATE: 1998-01-14 EARLIER PRING DATE: 1998-01-27 EARLIER PRILOGATION NUMBER: 60/045,491 EARLIER FILING DATE: 1997-11-06
                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.3%; Score 39.2; DB 3;
3.9%; Pred. No. 0.026;
ive 97; Mismatches 101;
Query Match 9.4%; Score 44.2; DB 3; Best Local Similarity 87.0%; Pred. No. 0.00094; Matches 60; Conservative 0; Mismatches 8;
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APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROIEIN
TITLE OF INVENTION: PUSIONS
FILE REFERENCE: 00786/350007
CURRENT APPLICATION NUMBER: 05/035,963
EARLIER FILING DATE: 1999-02-05
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
8.3%; Score 39.2; DB 3; Length 289;
Best Local Similarity 3.9%; Pred. No. 0.026;
Matches 8; Conservative 97; Mismatches 101; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (1)...(289)
COTHER INFORMATION: n = A/T/C or G
US-09-244-796-17
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Search completed: September 26, 2003, 13:42:36 Job time: 74 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

September 26, 2003, 13:07:01; Search time 207 Seconds (without alignments) 5676.520 Million cell updates/sec Run on:

US-10-045-116-1

472
1 AGCCACCACCAGTGAGCCT.....ACGTTCCTGGAACTCAAGCA 472 Perfect score: Sequence:

IDENTITY_NUC Scoring table:

Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 1678620 segs, 1244745471 residues Searched:

3357240

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 100% Listing first 45 summaries

Published_Applications_NA:* ٠. Database

| 'Ggn2_6/ptodata/2/pubpna/US07_PUBCOMB.seg:*
| 'Ggn2_6/ptodata/2/pubpna/US07_PUBCOMB.seg:*
| 'Ggn2_6/ptodata/2/pubpna/US06_NEW_PUB.seg:*
| 'Ggn2_6/ptodata/2/pubpna/US06_NEW_PUB.seg:*
| 'Ggn2_6/ptodata/2/pubpna/US06_NEW_PUB.seg:*
| 'Ggn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seg:*
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| 'Ggn2_6/ptodata/2/pubpna/US08_PUBCOMB.seg:*
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| 'Ggn2_6/ptodata/2/pubpna/US09_PUBCOMB.seg:* /cgn2_6/ptodatu/2/pubpna/US09_NEW_PUB.seq:*/cgn2_6/ptodatua/2/pubpna/US10A_PUBCOMB.seq:*/cgn2_6/ptodatua/2/pubpna/US10B_PUBCOMB.seq:*/ /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:* 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description			U .	Sequence // Appli		Sequence I, Appli	Sequence 4, Appli	Sequence 1, Appli	Sequence 4, Appli	14,	Sequence 14, Appl	Sequence 25, Appl			- -i (sequence 9/812, A	Sequence 8715, Ap	,
SUMMARIES	ID	US-09-151-376-7	US-09-151-376-54	US-10-139-089-7	US-10-139-089-54	US-10-045-116-1	US-09-947-925A-4	US-09-822-634-1	US-08-382-80-1	TS-00-014-257-14	TE-00-014 251 24	US 10 04F 155 1-14	02-10-045-116-25	US-10-226-820-10	US-10-090-238-1	US-10-212-667-2	HS-10-027-632-07012	10 10 001 CO 0100	ST/8-789-770-0T-SO	
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	Sequence 340, App Sequence 86, Appl Sequence 20321. A	217	Sequence 177, App	Sequence 1/7, App Sequence 177, App	169,	169	Sequence 103, App	Sequence 311, App	Sequence 311, App	Sequence 311, App	Sequence 16, Appl	Sequence 1478, Ap	Sequence 20347, A	Sequence 13797, A	Sequence 210, App	Sequence 349, App	Sequence 486, App	Segmence 16466 A	Sequence 7704 as	Someone F Anni	Sequence 3, Appli Sequence 10292, A
		-			US-09-922-217-169	US-US-833-263-169 US-10-025-380-169	US-10-027-632-127633	US-09-920-300A-311	US-10-099-926-311	US-10-033-528-311	US-09-756-551A-16	US-09-815-343-1478	US-09-814-353-20347	US-10-198-846-13797	S-TO-3T	US-09-815-343-349	US-09-871-161-486	US-09-814-353-16466	US-10-198-846-7704	US-10-208-408-5	US-10-198-846-10292
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19.9 15.9 15.9	15.9	12.8	12.2	12.2	12.1	12.1	11.9	11.7	11.7	777	4.1.	17.0	20.0) F	# C	10.0	4.	0.6	0.6	0.6	0.6
94 75 75	67.8	60.6 59	57.6 57.6	57.6	57.2	57.2	26	55.4	4.55	4.00	0.4 4.0	20 13	51.6 51.6	49.0		* *	7.44	42.4	42.4	42.4	42.4
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ALIGNMENTS

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                                            APPLICANT: Henderson, D.R.
APPLICANT: Schuur, E.R.
TITLE OF INVENTED: 1 INSSUE SPECIFIC VIRAL VECTORS
FILE REPRENCE: 1380-0220
CURRENT APPLICATION NUMBER: 08/09/151,376
CURRENT FILING DAIE: 1998-09-10
EARLIER FILING DAIE: 1996-06-26
EARLIER PILING DATE: 1996-06-26
EARLIER PILING DATE: 1996-06-26
EARLIER FILING DATE: 1996-06-27
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTING DAYE: 1995-06-27
Sequence 7, Application US/09151376 Publication No. US20030044383A1
                                                                                                                                                                                                                                                                                                                                                                                                             Matches 472; Conservative
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Best Local Similarity
                                     GENERAL INFORMATION:
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SEQ ID NO 7
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                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                             CTHER INFORMATION: Description of Unknown Organism: Unknown US-09-151-376-54
                                                                                                                                                                                                                                                                     APPLICANT: Henderson, D.R.
APPLICANT: Schuur, E.R.
TITLE OF INVENTION: 1208021
CURRENT APPLICATION NUMBER: 05/09/151,376
CURRENT APPLICATION NUMBER: 05/09/151,376
CURRENT FILING DAIE: 1996-09-10
BARLIER PEPLICATION NUMBER: 08/69,753
EARLIER FILING DAIE: 1996-06-26
EARLIER PELLING DAIE: 1996-06-27
NUMBER OF SEQ ID NOS: 71
                                                                                                                                                                                                                                        Sequence 54, Application US/09151376 Publication No. US20030044383A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                US-09-151-376-54
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LENGTH: 472
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Pred. No. 4.7e-137;
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Schuur, E.R.
TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
FILE REFERENCE: 346022000221
CURRENT APPLICATION NUMBER: US/10/139,089
CURRENT FILING DATE: 2002-05-05
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PRIOR APPLICATION NUMBER: 08/669,753

PRIOR FILING DATE: 1996-06-26

PRIOR FILING DATE: 1996-06-27

PRIOR FILING DATE: 1995-06-27

PRIOR FILING DATE: 1996-06-07

PRIOR FILING DATE: 1996-06-07

PRIOR PLICATION NUMBER: 09/509,591

PRIOR PLICATION NUMBER: 09/151,376

PRIOR PLICATION NUMBER: 09/151,376

PRIOR PLICATION NUMBER: 09/151,376

PRIOR PLICATION NUMBER: 09/033,428

PRIOR PLICATION NUMBER: 09/039,597

PRIOR FILING DATE: 1998-03-02

PRIOR FILING DATE: 1998-03-03

PRIOR FILING DATE: 1997-03-03

PRIOR FILING DATE: 1997-03-03

PRIOR FILING DATE: 1997-03-03

PRIOR FILING DATE: 1997-03-03

PRIOR FILING DATE: 1998-03-02

PRIOR PRILING DATE: 1998-03-02

PRIOR PRILING DATE: 1998-03-02

PRIOR PRILING DATE: 1998-03-02

PRIOR PRILING DATE: 1998-03-02
                                                                                                                                                                                                                                                Sequence 7, Application US/10139089; Publication No. US20030152553A1
CENERAL INFORMATION:
APPLICANT: Henderson, D.R.
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472; Conservative
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Best Local S:
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QY 241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGACAAAAGA 300 LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	D 42 ESULT 5 S-10-045-11 SEQUENCE 1. SEQUENCE 1. APPI CORF CORF CORF PRIC TELE TELE TELE SEQUENCE SEQU	9y 1 AGCCACCACGAGGGAGCCTTTTCTAGCCCCCAGAGCCACCTCTGTCGTGG 60
201 GGCAGAAATGAGGGGGGGACACCTGAATAAAGACCACCCATGACCA		Db 181 CAGAGGTCAGCACAGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCA

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GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGGACCCTGCTGGG
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APPLICANT: Huber, Brian
APPLICANT: Huber, Cynthia
APPLICANT: Richards, Cynthia
TITLE OF INVENTION: Antigen Regulatory
TITLE OF INVENTION: Sequence
TITLE OF INVENTION: Sequence
FILE REFERENCE: PBIO97033
CURRENT APPLICATION NUMBER: US/09/947,925A
CURRENT FILING DATE: 2001-09-06
PRIOR FILING DATE: 1993-11-19
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SOFTWARE: Patentin version 3.0
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Best Local Similarity
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APPLICANT: Harrington, Kevin
APPLICANT: Bateman, Andrew
APPLICANT: Murphy, Steven
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR TISSUE
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR TISSUE
ITILE OF INVENTION: SPECIFIC GENE REGULATION THERAPY
FILE REFERENCE: 07039-289001
CURRENT APPLICATION NUMBER: US/09/822,634
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 60/193,977
PRIOR PLILING DATE: 2000-03-31
MINMERS OF SECUENCE: NOW. 1000-03-31
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100.0%; Pred. No. 2.7e-136;
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Conservative 0; Mismatches
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1
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; Patent No. US20020150556Al
; GENERAL INFORMATION:
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471; Conserv
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                                                                                                   Sequence 4, Application US/09392822
Patent No. US20010053352A1
GENERAL INFORMATION:
APPLICANT: W. De Chao
APPLICANT: W. De Chao
APPLICANT: Henderson, Daniel
TITLE OF INVENTION: Adenovirus Vectors Containing Cell
TITLE OF INVENTION: Adenovirus Vectors Elements and Methods of Use Thereof
FILE REFERENCE: 348022001200
CURRENT APPLICATION NUMBER: US/09/392,822
EARLIER APPLICATION NUMBER: G0/099,791
EARLIER FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 9
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Pred. No. 3e-136;
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100.0%; Pre
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Publication No. US20030068307A1
GENERAL INFORMATION:
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ORGANISM: Homo Sapien
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US-09-392-822-4
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ITILE OF INVENTION: METHODS OF TREATING NEOPLASIA
TITLE OF INVENTION: MITH COMBINATION TARGET CELL-SPECIFIC ADENOVIRUS,
TITLE OF INVENTION: CHEMOTHERAPY AND RADIATION
FILE REFERENCE: 348022001600
CURRENT APPLICATION NUMBER: US/09/814,357
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 60/192,015
PRIOR FILING DATE: 2000-03-24
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COMPRISING AN INTERNAL RIBOSOME ENTRY SITE
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Pred. No. 3e-136;
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                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 15056
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PRIOR APPLICATION UNMER: 60/192,156
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 35
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Publication No. US20030148520A1
GENERAL INFORMATION:
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100.0%; Prr
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APPLICANT: Li, Yuanhao
APPLICANT: Henderson, Daniel R.
TITLE OF INVENTION: CELL-SPECIFIC,
TITLE OF INVENTION: COMPRISING AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.88;
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US-09-814-357-14
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les 471; Conservative
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TITLE OF INVENTION: TARGET CELL-SPECIFIC ADENOVIRAL VECTORS
TITLE OF INVENTION: CONTAINING E3 AND METHODS OF USE THEREOF
FILE REFERENCE: 348022001300
CURRENT APPLICATION NUMBER: US/10/226,820
CURRENT FILING DATE: 2002-08-21
                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                            REFERENCE/DOCKET NUMBER: 34802-30005.00
                                                                                                                                                                                                                                                                                                                                         99.8%; Score 471; DB 14; 100.0%; Pred. No. 3e-136;
                           APPLICATION NUMBER: US/09/033,555A
                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 25
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PRIOR APPLICATION NUMBER: US/09/474,699
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 60/114,262
                                                                             NAME: POLIZZI, CATHERINE M. REGISTRATION NUMBER: 40,130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/10226820 Publication No. US20030118555A1 GENERAL INFORMATION: APPLICANT: Henderson, Daniel R. APPLICANT: Yu, De Chao
                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
<Unknown>
                                              FILING DATE: 02-Mar-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                            TELEFAX: (415) 494-0792
TELEX: 706141 MRSNFOERS
                                                                                                                                                                                                                              LENGIH: 15056 base pairs
                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
             PRIOR APPLICATION DATA:
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CLASSIFICATION:
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EXPRESSING CARCINOEMBRYONIC ANTIGENS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGAGGACGACA 14481
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                                                                                                                                                                                     0;
                                                                                                                                                   99.8%; Score 471; DB 12; Length 15056; 100.0%; Pred. No. 3e-136;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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FILING DATE: 23-Oct-2001
                                                                                                                                                                                       Mismatches
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CORRESPONDEMCE ADDRESS:
ADDRESSEE: WORRISON & FORKSTER
STREET: 755 PAGE MILL ROAD
      SOFTWARE: FastSEQ for Windows Version 4.0
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Henderson, Daniel
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                                                                      ORGANISM: Artificial Sequence
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                                                                                                        CTHER INFORMATION: CEA TRE US-09-814-351-14
                                                                                                                                                        Query Match 99.8
Best Local Similarity 100.
Matches 471; Conservative
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                        SEQ ID NO 14
LENGTH: 15056
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                                                      TYPE: DNA
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                                                                                                   Score 471; DB 14; Length 15056; Pred. No. 3e-136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/10090238
Publication No. US20030176377A1
GENERAL INFORMATION:
APPLICANT: The Scripps Research Institute
APPLICANT: Relaph A. Resisfeld
TITLE OF INVENTION: LIGAND AND METHODS OF USE THEREOF
FILE REFERENCE: TSR.-830.0
CURRENT APPLICATION NUMBER: US/10/090,238
CURRENT FILING DATE: 2002-03-02
NUMBER OF ESQ. ID NOS: 3
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Pred. No. 2e-124;
0; Mismatches 1; ]
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Mismatches
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 15056
TYPE: DNA
ORGANISM: Homo Sapien
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                                                                                           99.8%; Scur-
100.0%; Pre-
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98.9%;
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                                                                           US-10-226-820-10
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Best Local S:
Matches 467
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Publication No. US20030082722A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: PROMOTEN
TITLE OF INVENTION NUMBER: US/10/212,667
PRIOR FILING DATE: 2001-08-08
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
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                                                                 121 ITTCTCTGTCACAAAGGAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG
                                        GGCATCATCCCACCTTCCCAGAGCCCTGGAGGATGGGGAGACCCGGGACCCTGCTGGG
                                                                                                                                                                                                      181 CAGAGGICAGCACIGGGG-AAGACAGGITGICCICCCAGGGGAIGGGGGICCAICCACCI
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                                                                                                                                                                                                                                                                                                                                                                    AGGCAGAAATGAGGGGGGGGGGGGGACAGACACCTGAATAAAGACCACACCCATGACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 AATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAGCAGAGGTCAGCACTGGGG-AAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.2%; Score 350.4; DB 14; Length 425; 98.7%; Pred. No. 3.7e-99; live 0; Mismatches 1; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence:; OTHER INFORMATION: Primer US-10-212-667-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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                                                                                                      AACTGAAAATAGAAGGGAAAAAAGAGGAGGACAAAAGAGGCAGAAATGAGAGGGGAGGG 237
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                                                                      GACAGAGGACACCTGAATAAAGACCACACCCATGACCCACGTGATGCTGAGAAGTACTCC
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, David G. TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28;
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Pred. No. 2.2e-27;
); Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                              GCCTTGACAAACGTTCCTGGAACTCAAGC 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR PRILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 1200-02-24
PRIOR PLICATION NUMBER: US 60/167,363
PRIOR PLICATION NUMBER: US 60/167,363
PRIOR PLICATION NUMBER: US 60/167,363
PRIOR PRILING DATE: 1999-11-23
PRIOR PRILING DATE: 1999-11-23
PRIOR PRILING DATE: 1999-09-28
PRIOR PRILING DATE: 1999-09-28
PRIOR PLILING DATE: 1999-09-28
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66.1%;
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Best Local Similarity 66.1
Matches 292; Conservative
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US-10-027-632-97812
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US-10-027-632-97812
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Search completed: September 26, 2003, 14:38:44 Job time: 209 secs

Page 1

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September 26, 2003, 12:16:11; Search time 2041 Seconds (without alignments) 5620.633 Million cell updates/sec
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472
1 AGCCACCACTGAGGCT.....ACGTTCCTGGAACTCAAGCA 472
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                  OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                             IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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                                                                                                        Run on:
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Se: EST:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	AW449279 UI-H-BI3- AZ53789 RPCI-23-1 AZ377232 IM0131P23 AL602851 DKFZp686P						
SUMMARIES	נו	AW449279 AZ553789 AZ377232 AL602851						
	DB	9 8 8 8						
	Query Match Length DB	328 522 588 595						
d¥	Query	87.8 18.6 75.2 15.9 71 15.0 69 14.6						
	Score	87.8 75.2 71 69						
	Result No.	H C7 CC 4						

0869 AU140869 29043 K-EST010 36430 K-EST010 52482 K-EST001 51932 K-EST002 51932 K-EST010 28560 K-EST010 28560 K-EST010			CB995910 AGENCOURT CB989395 AGENCOURT AL107519 Drosophil BX44199 BX44199 BX445657 BX445657 BX35916 BX359916 BX479971 HOMO SAPI BX479759 HOMO SAPI	6 4 5 7 7 7 8 2 8 2 7 8 2 8 2 9 8 2
9 AU1408 12 BM822 12 BM836 12 BM75 12 BM75 12 BM75 12 BM828 12 BM828 12 BM836 12 BM836 12 BM836 12 BM836 12 BM836 13 BM836 14 BM836 15 BM836 17 BM836 18 BM8	10000110	NHHH ABBE		, 44044444
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ALIGNMENTS

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Location/Qualifiers
                                                  Mus musculus (house mouse)
GI:11233609
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  AZ553789.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δy
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                                                                                                                                                                                                                                       /clone_11b="WorLcGAP_Sub5"
//clone_11b="WorLcGAP_Sub5"
//clone_11b="WorLcGAP_Sub5
is a subtracted library derived from NCI_CGAP_sub5
is a subtracted library derived from NCI_CGAP_sub4. The
NCI_CGAP_Sub5 library derived from NCI_CGAP_sub4 was used
as a tracer in a subtractive hybridization with a driver
comprising: the IMAGE pool (NCI_CGAP_Rib4 was used
as a tracer in a subtractive hybridization with a driver
comprising: the IMAGE pool (NCI_CGAP_Rib4 pool | LiAM
334-337, 3682-3683, 3798-3803 (IMAGE CloneIDS
1322776-1223911, 1456008-145675,1500525-1502885);
NCI_CGAP_Kid5 pool | LLAM 3338-3342,3722-3725, 3776-3778
[IMAGE CloneIDS | 1225831, 1471368-1472903,
1492104-1493255); NCI_CGAP_Lib5 pool | LLAM 2457-2459,
3851-3854 (IMAGE CloneIDS | 1414920-1417991, 1520904-152439
); NCI_CGAP_CGAP_Lib5 pool | LLAM 2457-2459,
3733-3735 (IMAGE CloneIDS | 144920-1417991, 1520904-152439
); NCI_CGAP_GOOL | LLAM 3164-3167, 3716-3720,
3733-3735 (IMAGE CloneIDS | 1227968-1286831, 1446964-1470983,
110192-1101959, 12217928-122050615); NCI_CGAP_COOL |
LLAM 2644-2653, 2871-2872 (IMAGE CloneIDS | 1057416-1061255,
1144584-1145351). (10% of the driver population), plus a pool of 3,840 arrayed clones from NCI_CGAP_Sub3 (IMAGE CloneIDS 2710535) and wcl_cGaP_Sub3 (IMAGE CloneIDS 2710535) and wcl_cGaP_Sub3 (IMAGE CloneIDS 2710535) and wcl_cGaP_Sub3 (IMAGE CloneIDS 2710536-2712859) (10% of the driver population), plus a pool of 5,472 clones from NCI_CGAP_Sub3 (IMAGE CloneIDS 2712456-272859) (10% of the driver population), plus a pool of 5,472 clones from NCI_CGAP_Sub3 (IMAGE CloneIDS 2712456-272859) (10% of the driver population), plus a pool of 5,472 clones from NCI_CGAP_Sub3 (IMAGE CloneIDS 2712456-272859) (10% of the driver population), plus a pool of 5,472 clones from NCI_CGAP_Sub3 (IMAGE CloneIDS 2712456-272859) (10% of the driver population), plus a pool of 5,472 clones from NCI_CGAP_Sub3 (IMAGE CloneIDS 2712456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FPCI-23-177H11.TJ RPCI-23 Mus musculus genomic clone RPCI-23-177H11 , genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCATCATCCCACCTTCCCAGAGCCCTGGAGGATGGGGAGACCCGGGACCCTGCTGGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---TGTGACAG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 AGTCATCCCCCAGTGAGCCCCTTTCCATCCCCCAGAGCCACCTCTGTCACCTTCCTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 TIGCAAAGAAAATAATTACCACATTIGGATATGCCAGGGTTCTCTGTGTGCTGCTGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AGCCACCACCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 ACCCAAGGACAGAACACAGCAGAGGICAGCACTGGGGAAGACAGGITGICCICCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8e-09;
-hes 62; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 328;
                                                                                                                                                                                                  /lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_Sub5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 87.8; D
Pred. No. 8e-0
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 TITCICIGICACAAAGAAAAAAATAATCCCCTGG~
                                                                                          /organism="Homo sapiens"
                                                                                                                                             /db_xref="taxon:9606"
/clone="IMAGE:2734193"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Research 6, 791-806.
TAG_LIB=NCI_CGAP_Col0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 9
                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAG_TISSUE=colon
TAG_SEQ=AAACG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.6%;
65.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ಥ
              POLYA-Yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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AZ553789
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
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ACCESSION

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/lab_host="DH10B"
//clone_lib="RPCI-2"
//clone_lib="RPCI-2"
//note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
FooRI; Site_2: EcoRI; Female C57BI/6J mouse kidney and/or
Broin genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
BH10B electrocompetent cells (BRL Life Technologies).

a 119 c 136 g 132 t
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                                                                                                                                                                                                                                                                                                                                                                                                                             Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/hac_ends/mouse/bac_end_intro.html Seq primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 GCCCIGGAGAGCATGGGGAAGACCCGGGACCCTGCTGGGTTTCTCTGTCACAAAGGAAAAT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247 AAGATTIGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGGGAGGAGGACAAAAAGAGGCAGA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhao'.'. Nierman,W'.' Feldblyum,T'. Malek,J'.' Shatsman,S'. Akinret,B., Levins,M., Mcgann,S'.' Tsegaye,G'.' Geer,K'.' Krol,M'.' de Jong,P. and Fraser,C'.M'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---TGACAGACCCAAGGACAGAACACAGAGGG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 AGGAAGGATCCCTCTTGATGCTGACAGACTCATGTCCAGGAGTCAGCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 IICTAGCCCCCAGAGCCACCICIGICACCTICCIGIIGGGCAICAICCCACCTICCCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              270 ICAGCGCCTGGATGATCATTGTTCTCTGAGGCATGTCGATACTTATCATCTGTGTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                              MD 20850,
                                                                                                                                                                                 Mouse BAC End Sequences from Library RPCI-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.9%; Score 75.2; DB 28; 55.9%; Pred. No. 4e-06; Live 0; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                           9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                Unpublished
Other GSSs: RPCI-23-177H11.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="RPCI-23-177H11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \nabla
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BASE COUNT ORIGIN Query Me Best Loc Matches	QY	ζ δ pp	Qy Db	QY	Qy	QY Db	QY QU	δŏ	Db RESULT 4 AL602851	LOCUS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES
307 AATGAGGGGGGGGACAGAGGACACCTGAATAAAGACCACCCCATGACCCAC 361 390 ACTGAGAGGGAAGTGACTGAGTGGTCACAGACCCACACACA	509 CACA 512	AZ377232 N 1M0131P23F Mouse 10kb plasmid UUGCLM library Mus musculus genemic	clone UUGClM0131P23 F, genomic survey sequence. A2377232.1 GI:10490932 GSS.	Mus musculus (house mouse) Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wridth, D., Weiss, R.	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished		84112, USA Tel: 801 585 5606 Fax: 801 585 7177	Email: ddunn@genetics.utah.edu Insert Length: 10000	High qual		/lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-" /clone_lib="Mouse lokb plasmid UGCIM library" /note="Vector: PWD42nv; Purified genomic DMA from M. musculus C57BL/G (male) was obtained from the Jackson Laboratory Wouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T H DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The	adaptored by was putilised and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of phya2 (gil4732114)gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
Qy Db Qy Db	qq	RESULT 3 AZ377232 LOCUS DEFINITION	ACCESSION VERSION KEYWORDS	SOURCE ORGANISM REFERENCE	AUTHORS	TITLE	COMMENT			FEATURES			

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4
chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

129 c 162 g 139 t l others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         595 bp mRNA linear EST 14-AUG-2001
DKFZp686F1216_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
AL602851
                                                                                                                                                                                                                                                  155
                                                                                                                                                                                                                                                                                              142
                                                                                                                                                                                                                                                                                                                                                                           ----TGACAGACCCAAGGACAGAACACAGCAGAGG 186
                                                                                                                                                                                                                                                                                                                                                                                                                          275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 AAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGAGGAGGCACAAAAGAGGCAGA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 ICAGCCCTTGGAIGAGTTGTTGTTGTGAGGGCATGCCGATGCTTATCAGCCTTGTTGC 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         307 AATGAGAGGGAGGGACAGAGGACACCTGAATAAAGA-----CCACACCCATGACCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 595)
Wambutt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.
EST (Wambutt,R., Heubner,D., Mewes,H.W., Weil,B. and Wiemann,S.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKEZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
Consortium of the German Genome Project.
This clone (DKFZp686P1216) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@tzpd.de.
                                                                                                                                                                                            23 TTCTAGCCCCCAGAGCCACCTCTTCTTCTGTTGGGCATCATCCCACGAGA
                                                                                                                                                                                                                     83 GCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGGTTTCTCTGTCACAAAGGAAAAT
                                                                                                                                                                                                                                                                                                           216 AGGAATGATGGAGGCICCCTCTTTGATGCTGACAGACTCATATCTGGGAGTCAGCATATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                      187 ICAGCACIGGGGAAGACAGGIIGTCCICCCAGGGGAIGGGGGICCATCCACCITGCCGAA
                                                                                                                                                            24; Gaps
                                                                                                                   Length 588;
                                                                                                        Score 71; DB 28; Length 588
Pred. No. 3.2e-05;
0; Mismatches 166; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL602851.1 GI:15166357
                                                                                                            15.0%;
55.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                    143 AATCCCCCTGGTG----
                                                                                                                            ocal Similarity 55.2
s 234; Conservative
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2 AAATGTAGACAGAAGGGAGAAAGGAAGAAGAAAATGAGGCAAAAACTGAGAGGGGAGGG
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix

Research Institute; cDNA library construction: Department of

Virology, Institute of Medical Science, University of Tokyo, and

Helix Research Institute.
                                                                                         /lab_nost="pH10B"
/clone_lb="686 (synonym: hlcc3)"
/note="vector: pTriplEx2; Site_1: SfilA; Site_2: SfilB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sugiyama, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases I to 787)
Ota, T., Suzuki, Y., Salto, K., Ishli, S., Yamamoto, J., Sugiyama, T.
Nishikawa, T., Nakamura, Y., Sugano, S., Masuho, Y. and Isogai, T.
HRI human cDNA project (Ota, T., Suzuki, Y., Salto, K., Ishli, S., Masuho, Y., Isogai, T., Mishikawa, T., Nakamura, Y., Sugano, S., Masuho, Y., Isogai, T., Nishikawa, T., Nakamura, Y., Sugano, S., Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262 AACTGAAAATAGAAGGGAAAAAAGAGGAGGACAAAAAGAGGCAGAAATGAGAGGGGAGGG
                                                                                                                                                                                                                                                 0; Gaps
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                      /db_xref="taxon:9606"
/clone="DKFZp686P1216"
/tissue_type="human skeletal muscle"
/dev_stage="admit"
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
                                                                                                                                                                                                             14.6%; Score 69; DB 9; Li
ilarity 100.0%; Pred. No. 8.6e-05;
Conservative 0; Mismatches 0;
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Pred. No. 9.4e-05;
0; Mismatches 72
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1 205 c 203 g 1444
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            /mol_type="mRNA"
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AU140869.1 GI:11002390
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61.9%;
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Genomics Laboratory
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Best Local Similarity
Matches 69; Conserv
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/actor_lib="SoynGot"
/force="Organ: Stomach: Vector: pME18-FL3; Site_1: XhoI;
/force="Organ: Stomach: Vector: pME18-FL3; Site_1: XhoI;
/site_2: XhoI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including SiII
site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized with Superscript II using SfII
oligo-dT primer. After first strand synthesis, RNA was
degraded by NaoH treatment and cDNA was amplified by PCR
reaction. The PCR products were digested with Stil and
                                                                                                                                                                                                                                                                                                                                                               {\tt BM829043} 220~{\tt bp} mRNA linear EST 06-MAR-2002 K-EST0101950 S9SNU601 Homo sapiens cDNA clone S9SNU601-52-B11 5', mRNA sequence.
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                                                                                                                            62 GACAGAGAGGTGACCTGGGCAGAGCTTCACC-----CATGACCTGGAAAGTGCTCC 113
                                                                                             322 GACAGAGGACACCTGAATAAAGACCACCCCATGACCCACGTGATGCTGAGAAGTACTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: Yongsung@mail.kribb.re.kr
Plate: 52 row: B column: 11
High quality sequence stop: 220.
Location/Qualiflers
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/lab_host="roplog".
//lab_host="roplog".
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K-EST0029023 S9SNU601 Homo sapiens cDNA clone S9SNU601-6-B10 5',
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1 (Dases 1 to 279)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
                     105 AGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAA 464
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                                                         Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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100.0%; Pred. No. 0.00024;
tive 0; Mismatches 0;
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High quality sequence stop: 279.
Location/Qualifiers
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Plate: 6 row: B column: 10
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Contact: Kim YS
Genome Research Center
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Matches 67; Conserv
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K-EST0112089 $95NU601 Homo sapiens cDNA clone $95NU601-61-B06 5',
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1 (bases 1 to 275)
Kim, N. S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.S., Hahn, Y., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
21C Frontier Korean EST Project 2001
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                                                                                 405 AGAGGGAGGAAGGACGAGCCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAA 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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Contact: Kim YS
Genome Research Center
Genome Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-8
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/clone="S9SNU601-61-B06"
         Pred. No.
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/cell_line="SNU-601"
/lab_host="Top10F'"
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100.0%;
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/clone_lib="SSSNUG01"
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/rhe competent_cells E. coli Topl0F' by electroporation method
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                                                                                                                                                                            BM836104 355 bp mRNA linear EST 06-MAR-2002 K-EST011597 S9SNU601 Homo sapiens CDNA clone S9SNU601-65-F08 5', mRNA sequence.
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Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Ecoun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-44409
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14.2%; Score 67; DB 12; Length 355;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 67; Conservative 0; Mismatches 0; Indels
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Plate: 65 row: F column: 08
High quality sequence stop: 355.
Location/Qualifiers
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BM751932 418 bp mRNA linear EST 04-MAR-2002
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1 (Dases I to 418)

Kim, N. S., Hahn, Y., Oh, J. H., Lee, J. Y., Ahn, H. Y., Chu, M. Y., Kim, M. R., Oh, K. J., Cheong, J. E., Sohn, H. Y., Kim, J. M., Park, H. S., Kim, S. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Beoun-dong-qu, Daejeon 305-333, South Korea
Far: +82-42-860-4470
Fax: +82-42-860-4409
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21C Frontier Korean EST Project 2001
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Plate: 18 row: E column: 04
High quality sequence stop: 418
Location/Qualifiers
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Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
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Fat: +82-42-860-4470
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Homo sapiens (human)
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/cell_type="Bpithelial"
/cell_line="SNU-601"
/lab_host="Toplog" "
/colone_lib="S9SNU601"
/rote="Organ: Stomach; Vector: pME18-FL3; Site_l: Xho!;
/rote="Organ: Stomach; Vector: pME18-FL3; Site_l: Xho!
/rote="Organ: Stomach; Vector was dephosphorylated with
/rote organ: Stomach; Vector with Superscript II using Sfil
/rote organ: After first strand synthesis, RNA was
/rote organ: After first strand
/rote organ: After first s
                                                         HANZESSO 483 bp mRNA linear EST 06-MAR-2002 R-EST0101388 S9SNU601 Homo sapiens cDNA clone S9SNU601-53-D01 5', mRNA sequence.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 483)
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Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Ecenn-dong Yusecng-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="S9SNU601-53-D01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: yongsung@mail.kribb.re.kr
Plate: 53 row: D column: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plate: 53 row: D column: 01
High quality sequence stop: 483.
Location/Qualifiers
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/mol_type="genomic DNA"
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Location/Qualifiers
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Homo sapiens (human)
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/lab_host="TopOlOF"
/lab_host="TopOlOF"
/clone_lib="S9SNUG01"
/clone_lib="S9SNUG01"
/clone_lib="S9SNUG01"
/clone_lib="S9SNUG01"
/site_2: Xhoi: The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including Sfil site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using Sfil olygo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with Sfil and cloned into Draill- digested pMB18S-Fi3 vector. The obtained cDNA vectors were used for transformation of competent cells E. coli ToplOF' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
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HS_2278_A2_A04_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2278 Col=8 Row=A, genomic survey
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Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                         Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eceun-Gong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mall.krlbb.re.kr
Plate: 4 row: E column: 04
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Unpublished
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/db_xref="taxon:9606"
/clone="S9SNU601-4-E04"
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Location/Qualifiers
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    BM752131.1 GI:19081749
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                                            Homo sapiens (human)
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1 (bases I to 195)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brenteni, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW839587 18-MAY-2000 RC6-LT0072-020200-021-B10 LT0072 Homo sapiens CDNA, mRNA sequence. AW839587
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 879) Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Roller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 195)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2278 row: A column: 8
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University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
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Site_l: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
31 a 46 c 67 g 51 t
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Fax: +55-11-2707001
Bmail: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC6-LT0072-020
200-021-BloG0-02-02&t4=1)
Seq primer: puc 18 forward
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
  Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
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                                               Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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